SEQUENCE LISTING

<110> Leng, Jay

<120> PROTEASE SPECIFIC CLEAVABLE LUCIFERASES AND METHODS OF USE THEREOF

<130> 105175-159907

<140> Not Yet Known
<141> 2000-07-19

<160> 29

<170> PatentIn Ver. 2.1

<210> 1
<211> 936
<212> DNA
<213> Renilla reniformis

<220>
<221> CDS
<222> (1)..(936)

<400> 1

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atg act tcg aaa gtt tat gat cca gaa caa agg aaa cgg atg ata act   48
Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
  1               5                  10                  15

ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca   96
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
             20                  25                  30

ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att   144
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
         35                  40                  45

ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg   192
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
     50                  55                  60

cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt   240
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
 65                  70                  75                  80

atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat   288
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
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                    85                  90                  95

cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag   336
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
            100                 105                 110

aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat   384
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
        115                 120                 125

tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa   432
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
    130                 135                 140

agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa   480
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145                 150                 155                 160

gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg   528
Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
                165                 170                 175

gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga   576
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
            180                 185                 190

aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca ttc aaa gag   624
Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
        195                 200                 205

aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg   672
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
    210                 215                 220

tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat   720
Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
225                 230                 235                 240

aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa   768
Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
                245                 250                 255

tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag   816
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
            260                 265                 270

ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa   864
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
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        275                 280                 285

gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag   912
Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
    290                 295                 300

cga gtt ctc aaa aat gaa caa taa                                   936
Arg Val Leu Lys Asn Glu Gln
305                 310
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<210> 2
<211> 311
<212> PRT
<213> Renilla reniformis

<400> 2

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Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
  1               5                  10                  15
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
             20                  25                  30
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
         35                  40                  45
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
     50                  55                  60
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
 65                  70                  75                  80
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
                 85                  90                  95
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
            100                 105                 110
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
        115                 120                 125
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
    130                 135                 140
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145                 150                 155                 160
Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
                165                 170                 175
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
            180                 185                 190
Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
        195                 200                 205
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
    210                 215                 220
Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
225                 230                 235                 240
Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
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```
                245                 250                 255
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
            260                 265                 270
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
        275                 280                 285
Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
    290                 295                 300
Arg Val Leu Lys Asn Glu Gln
305                 310
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<210> 3
<211> 936
<212> DNA
<213> Renilla reniformis (mutated sequence)

<220>
<221> CDS
<222> (1)..(936)

<400> 3

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atg act tcg aaa gtt tat gat cca gaa caa agg aaa cgg atg ata act   48
Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
  1               5                  10                  15

ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca   96
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
             20                  25                  30

ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att   144
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
         35                  40                  45

ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg   192
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
     50                  55                  60

cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt   240
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
 65                  70                  75                  80

atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat   288
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
                 85                  90                  95

cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag   336
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
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```
            100                 105                 110

aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat   384
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
        115                 120                 125

tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa   432
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
    130                 135                 140

agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa   480
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145                 150                 155                 160

gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg   528
Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
                165                 170                 175

gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga   576
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
            180                 185                 190

aag tta gaa cca gac gaa gtt gac gca tat ctt gaa cca ttc aaa gag   624
Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu
        195                 200                 205

aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg   672
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
    210                 215                 220

tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat   720
Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
225                 230                 235                 240

aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa   768
Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
                245                 250                 255

tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag   816
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
            260                 265                 270

ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa   864
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
        275                 280                 285

gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag   912
Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
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    290                 295                 300

cga gtt ctc aaa aat gaa caa taa                                        936
Arg Val Leu Lys Asn Glu Gln
305                 310


<210> 4
<211> 311
<212> PRT
<213> Renilla reniformis (mutated sequence)

<400> 4
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Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
             20                  25                  30
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
         35                  40                  45
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
     50                  55                  60
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
 65                  70                  75                  80
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
                 85                  90                  95
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
            100                 105                 110
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
        115                 120                 125
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
    130                 135                 140
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145                 150                 155                 160
Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
                165                 170                 175
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
            180                 185                 190
Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu
        195                 200                 205
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
    210                 215                 220
Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
225                 230                 235                 240
Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
                245                 250                 255
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
            260                 265                 270
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
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        275                 280                 285
Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
    290                 295                 300
Arg Val Leu Lys Asn Glu Gln
305                 310
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<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease recognition sequences

<400> 5
Ser Gln Asn Tyr Pro Ile Val Gln
1 5

<210> 6
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease recognition sequences

<400> 6
Lys Ala Arg Val Leu Ala Glu Ala Met Ser
1 5 10

<210> 7
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease recognition sequences

<400> 7
Pro Ser Pro Arg Glu Gly Lys Arg Ser Tyr
1 5 10

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 8
Tyr Val Ala Asp Gly
1 5

<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 9
Met Phe Gly Gly Ala Lys Lys Arg
1 5

<210> 10
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 10
Gly Val Val Asn Ala Ser Ser Arg Leu Ala
1 5 10

<210> 11
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 11
Leu Ile Ala Tyr Leu Lys Lys Ala Thr
1 5

<210> 12
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 12
Val Lys Met Asp Ala Glu Phe
1 5

<210> 13
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 13
Phe Leu Ala Glu Gly Gly Gly Val Arg Gly Pro Arg Val Val Glu Arg
1 5 10 15

His

<210> 14
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease

recognition sequences

<400> 14
Asp Arg Val Tyr Ile His Pro Phe His Leu Val Ile His
1 5 10

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease recognition sequences

<400> 15
Lys Pro Ala Leu Phe Phe Arg Leu
1 5

<210> 16
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease recognition sequences

<400> 16
Ile Glu Pro Asp
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<210> 17
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease recognition sequences

<400> 17
Asp Glu Thr Asp
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<210> 18
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 18
Trp Glu His Asp
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<210> 19
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 19
Tyr Val Ala Asp
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<210> 20
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 20
Asp Glu His Asp
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<210> 21
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 21
Asp Glu Val Asp
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<210> 22
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> X at residue 1 is W or L

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 22
Xaa Glu His Asp
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<210> 23
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> X at residue 3 is I or H

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 23
Val Glu Xaa Asp
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<210> 24
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 24
Leu Glu Thr Asp
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<210> 25
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 25
Leu Glu His Asp
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<210> 26
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> X at residues 1 to 3 can be any amino acid

<220>
<223> Description of Artificial Sequence: Protease
recognition sequences

<400> 26
Xaa Xaa Xaa Asp
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<210> 27
<211> 8
<212> PRT
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<400> 27
Arg Pro Leu Gly Ile Ile Gly Gly
1 5

<210> 28
<211> 3
<212> PRT
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<220>
<223> Description of Artificial Sequence: Protease recognition sequence

<400> 28
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<210> 29
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protease recognition sequence

<400> 29
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